STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/555,735_

Source: _IFWO_

Date Processed by STIC: _12/04/2006_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _10/555,735_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length — The rules require that a line **not exceed 72** characters in length. This includes white spaces.

3_____Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4_____Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length — Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue n or Xaa represents.

10_____Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11_____Use of <220> — Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12_____PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa — "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/555,735

DATE: 12/04/2006
TIME: 12:59:05

Input Set : N:\efs\12_04_06\10555735_efs\INTM01901USseqlist.txt
Output Set: N:\CRF4\12042006\J555735.raw

```
 4 <110> APPLICANT: Blatt, Lawrence M.
 6 <120> TITLE OF INVENTION: SYNTHETIC CHEMOKINE RECEPTOR LIGANDS AND
 7       METHODS OF USE THEREOF
 9 <130> FILE REFERENCE: INTM-033WO
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/555,735
C--> 12 <141> CURRENT FILING DATE: 2005-11-07
14 <150> PRIOR APPLICATION NUMBER: 60/471,404
15 <151> PRIOR FILING DATE: 2003-05-16
17 <160> NUMBER OF SEQ ID NOS: 20
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 77
23 <212> TYPE: PRT
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: consensus IP-10 sequence
29 <400> SEQUENCE: 1
30 Val Pro Leu Ser Arg Thr Gly Arg Cys Thr Cys Ile Ser Ile Ser Asn
31 1               5                  10                  15
32 Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu Glu Ile Ile Pro Pro
33              20                  25                  30
34 Ser Gln Phe Cys Pro Lys Ile Glu Ile Ile Ala Thr Leu Lys Lys Asn
35           35                  40                  45
36 Gly Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys Ala Ile Lys Asn Leu
37        50                  55                  60
38 Ile Lys Lys Val Ser Arg Glu Met Ser Lys Lys Ser Pro
39 65                  70                  75
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 74
44 <212> TYPE: PRT
45 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
48 <223> OTHER INFORMATION: consensus I-TAC sequence
50 <400> SEQUENCE: 2
51 Phe Pro Met Phe Arg Arg Gly Arg Cys Leu Cys Ile Ser Pro Gly Val
52 1               5                  10                  15
53 Lys Ala Val Lys Val Ala Ser Leu Glu Lys Leu Ser Ile Met Tyr Pro
54              20                  25                  30
55 Ser Asn Asn Cys Asp Lys Ile Glu Ile Ile Ala Thr Leu Lys Lys Asn
56           35                  40                  45
57 Gly Gly Gln Arg Cys Leu Asn Pro Lys Ser Lys Gln Ala Lys Leu Leu
58        50                  55                  60
59 Ile Lys Lys Val Glu Arg Lys Lys Asn Phe
```

*Does Not Comply
Corrected Diskette Needed*

(P3 - 3)

```
60 65                    70
63 <210> SEQ ID NO: 3
64 <211> LENGTH: 104
65 <212> TYPE: PRT
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: consensus Mig sequence
71 <400> SEQUENCE: 3
72 Thr Pro Val Val Arg Lys Gly Arg Cys Ser Cys Ile Ser Thr Asn Gln
73 1                   5                   10                  15
74 Gly Thr Val His Leu Gln Ser Leu Glu Lys Leu Lys Ile Phe Ala Pro
75              20                  25                  30
76 Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile Ala Thr Leu Lys Lys Asn
77          35                  40                  45
78 Gly Val Gln Arg Cys Leu Asn Pro Asp Ser Lys Asp Val Lys Glu Leu
79      50                  55                  60
80 Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys Lys Lys Gln Lys Asn
81 65                  70                  75                  80
82 Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys Val Arg Lys Val Gln
83              85                  90                  95
84 Arg Ser Arg Gln Lys Lys Thr Thr
85              100
88 <210> SEQ ID NO: 4
89 <211> LENGTH: 10
90 <212> TYPE: PRT
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: epitope tag
96 <400> SEQUENCE: 4
97 Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
98 1                   5                   10
101 <210> SEQ ID NO: 5
102 <211> LENGTH: 8
103 <212> TYPE: PRT
104 <213> ORGANISM: Artificial Sequence
106 <220> FEATURE:
107 <223> OTHER INFORMATION: epitope tag
109 <400> SEQUENCE: 5
110 Asp Tyr Lys Asp Asp Asp Asp Lys
111 1                   5
114 <210> SEQ ID NO: 6
115 <211> LENGTH: 11
116 <212> TYPE: PRT
117 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
120 <223> OTHER INFORMATION: epitope tag
122 <400> SEQUENCE: 6
123 Cys Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
124 1                   5                   10
```

```
127 <210> SEQ ID NO: 7
128 <211> LENGTH: 5
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: protease cleavage site
135 <400> SEQUENCE: 7
136 Asp Asp Asp Asp Lys
137  1               5
140 <210> SEQ ID NO: 8
141 <211> LENGTH: 4
142 <212> TYPE: PRT
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: protease cleavage site
148 <400> SEQUENCE: 8
149 Ile Glu Gly Arg
150  1
153 <210> SEQ ID NO: 9
154 <211> LENGTH: 6
155 <212> TYPE: PRT
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: protease cleavage site
161 <400> SEQUENCE: 9
162 Leu Val Pro Arg Gly Ser
163  1               5
166 <210> SEQ ID NO: 10
167 <211> LENGTH: 8
168 <212> TYPE: PRT
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: protease cleavage site
174 <400> SEQUENCE: 10
175 His Pro Phe His Leu Val Ile His
176  1               5
179 <210> SEQ ID NO: 11
180 <211> LENGTH: 104
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Majority Sequence
W--> 187 <221> NAME/KEY: VARIANT
188 <222> LOCATION: 1, 3, 4, 6, 10, 14, 15, 16, 17, 18, 20, 21, 22, 28, 30, 31,
189        34, 35, 37, 50, 57, 60, 61, 63, 68, 69, 70, 71, 72, 73,
190        74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87,
191        88, 89, 90, 91, 92, 93, 94, 96, 98, 99, 100, 103, 104
192 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 194 <400> 11
```

Invalid Response. what is the source of genetic material. see Item 11 on Error Summary Sheet

RAW SEQUENCE LISTING   DATE: 12/04/2006
PATENT APPLICATION: US/10/555,735   TIME: 12:59:05

Input Set : N:\efs\12_04_06\10555735_efs\INTM01901USseqlist.txt
Output Set: N:\CRF4\12042006\J555735.raw

```
W--> 195 Xaa Pro Xaa Xaa Arg Xaa Gly Arg Cys Xaa Cys Ile Ser Xaa Xaa Xaa
     196  1               5               10              15
     197 Xaa Xaa Val Xaa Xaa Xaa Ser Leu Glu Lys Leu Xaa Ile Xaa Xaa Pro
     198              20              25              30
     199 Ser Xaa Xaa Cys Xaa Lys Ile Glu Ile Ile Ala Thr Leu Lys Lys Asn
     200          35              40              45
     201 Gly Xaa Gln Arg Cys Leu Asn Pro Xaa Ser Lys Xaa Xaa Lys Xaa Leu
     202      50              55              60
     203 Ile Lys Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     204 65              70              75                          80
     205 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa
     206              85              90                      95
     207 Arg Xaa Xaa Xaa Lys Lys Xaa Xaa
     208              100
     211 <210> SEQ ID NO: 12
     212 <211> LENGTH: 98
     213 <212> TYPE: PRT
     214 <213> ORGANISM: Homo sapien
     216 <400> SEQUENCE: 12
     217 Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
     218  1               5               10              15
     219 Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys
     220              20              25              30
     221 Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu
     222          35              40              45
     223 Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala
     224      50              55              60
     225 Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys
     226 65              70              75                          80
     227 Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Met Ser Lys Arg
     228              85              90                      95
     229 Ser Pro
     233 <210> SEQ ID NO: 13
     234 <211> LENGTH: 94
     235 <212> TYPE: PRT
     236 <213> ORGANISM: Homo sapien
     238 <400> SEQUENCE: 13
     239 Met Ser Val Lys Gly Met Ala Ile Ala Leu Ala Val Ile Leu Cys Ala
     240  1               5               10              15
     241 Thr Val Val Gln Gly Phe Pro Met Phe Lys Arg Gly Arg Cys Leu Cys
     242              20              25              30
     243 Ile Gly Pro Gly Val Lys Ala Val Lys Val Ala Asp Ile Glu Lys Ala
     244          35              40              45
     245 Ser Ile Met Tyr Pro Ser Asn Asn Cys Asp Lys Ile Glu Val Ile Ile
     246      50              55              60
     247 Thr Leu Lys Glu Asn Lys Gly Gln Arg Cys Leu Asn Pro Lys Ser Lys
     248 65              70              75                          80
     249 Gln Ala Arg Leu Ile Ile Lys Lys Val Glu Arg Lys Asn Phe.
     250              85              90
```

```
253 <210> SEQ ID NO: 14
254 <211> LENGTH: 125
255 <212> TYPE: PRT
256 <213> ORGANISM: homo sapien
258 <400> SEQUENCE: 14
259 Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val
260 1               5                   10                  15
261 Leu Ile Gly Val Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser
262             20                  25                  30
263 Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp
264         35                  40                  45
265 Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile
266     50                  55                  60
267 Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala
268 65                  70                  75                  80
269 Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys
270                 85                  90                  95
271 Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
272             100                 105                 110
273 Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
274             115                 120                 125
277 <210> SEQ ID NO: 15
278 <211> LENGTH: 98
279 <212> TYPE: PRT
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: hybrid CXCR3 ligand
285 <400> SEQUENCE: 15
286 Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val
287 1               5                   10                  15
288 Leu Ile Gly Val Gln Gly Phe Pro Met Phe Lys Arg Gly Arg Cys Leu
289             20                  25                  30
290 Cys Ile Gly Pro Gly Val Lys Pro Val Asn Pro Arg Ser Leu Glu Lys
291         35                  40                  45
292 Leu Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Ile Glu Ile Ile
293     50                  55                  60
294 Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Lys
295 65                  70                  75                  80
296 Gln Ala Arg Leu Ile Ile Lys Lys Val Ser Lys Glu Met Ser Lys Arg
297             85                  90                  95
298 Ser Pro
302 <210> SEQ ID NO: 16
303 <211> LENGTH: 124
304 <212> TYPE: PRT
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: hybrid CXCR3 ligand
310 <400> SEQUENCE: 16
311 Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/04/2006
PATENT APPLICATION: US/10/555,735   TIME: 12:59:06

Input Set : **N:\efs\12_04_06\10555735_efs\INTM01901USseqlist.txt**
Output Set: **N:\CRF4\12042006\J555735.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 1,3,4,6,10,14,15,16,17,18,20,21,22,28,30,31,34,35,37,50
Seq#:11; Xaa Pos. 57,60,61,63,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82
Seq#:11; Xaa Pos. 83,84,85,86,87,88,89,90,91,92,93,94,96,98,99,100,103,104

VERIFICATION SUMMARY   DATE: 12/04/2006
PATENT APPLICATION: US/10/555,735   TIME: 12:59:06

Input Set : **N:\efs\12_04_06\10555735_efs\INTM01901USseqlist.txt**
Output Set: **N:\CRF4\12042006\J555735.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:187 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:194 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11